

FIG. 1A

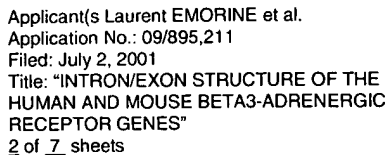


FIG. 1B



gatctgtaatccacgactgggaggtgagcagaaggtgaggtccagaccactctgggcaacatatagaagactatctcaacaataagatacattaggagagcatcccaagc 120
agaagagggctatcttgatggttgggttgcgttttgggttcttgatggttgccttctcttggtaagatagggtgcgggttctctcttcttgcaaggtt 240
gcctcaggttctgcaaggaaggtgctgagctccaggaaccgggtgctgagggagtgctcaagacagagccctctccacccctccaattcccaccagagggcctctcttgactatt 360
ggacgctgttctcttaaaagcagccactcctccggcaacttaggtgtacatgggggtgagatggaggaagctgacagacttaccacgaattagggaagatggcccaggctggaag 480
agtcgctcccaagccctactgtcccttccctaagccagcgggtctgaggagaggagggggaaccttccaccacccagcgccacacgag ATG GCT CCG TGG CCT CAC AGA AAC 591
M A P W P H R N 8
GGC TCT CTG GCT TTG TGG TCG GAC GGC CCT ACC CTG GAC CCC AGT GCA GCC AAC ACC AGT GGG TTG CCA GGA GTA CCA TGG GCA GCG GCA 681
G S L A L W S D A P T L D P S A A N T S G L P G V P W A A A 38
TTG GCT GGG GCA TTG CTG GCG CTG GCG AAC CTG GGA GGC AAC CTG CTG GTA ATC ATA GCC ATC GCC CGC AGC CCG AGA CTA CAG ACC ATA 771
L A G A L L A L A T V G N L L V I I A I A R T P R L Q T I 68
ACC AAC GTG TTC GTG ACT TCA CTG GCG GAA GCT GAC TTG GTA GTG GGA CTC CTC GTA ATG CCA CCA GGG GCC ACA TTG GCG CTG ACT GGC 861
T N V F V T S L A A A D L V G L L V M P G A T L A L T G 98
CAT TGG CCC TTG GCG GAA ACT GGT TGC GAA CTG TGG ACG TCA CTG GAC CTG CTC TGT GTA ACT GCT AGC ATC GAG ACC TTG TGC GCC CTG 951
H W P L G E T G C E L W T S V D V L C V T A S I E T L C A L 128
GCT GTG GAC CGC TAC GCT GTC ACC AAC CCT TTG CGT TAC GGC ACG CTG GTT ACC AAG CGC CGC GCG GCG GCA GTT GTC CTG GTG 1041
A V D R Y L A V T N P L R Y G T L V T K R A R A A V V L V 158
TGG ATC GTG TCC GCT GCC GTG TCC TTT GCG CCC ATC ATG AGC CAG TGG CGT GTA GGG GCA GAT GCC GAG GCA CAG GAA TGC CAC TCC 1131
W I V S A A V S F A P I M S Q W R V G A D A E A Q E C H S 188
AAT CCG CGC TGC TGT TCC TTT GCG TCC AAC ATG CCC TAT GCG CTG CTC TCC TCC TCC TCC TCC TCC TCC TCC TCC TCC TCC TCC TCC TCC TCC 1221
N P R C C S F A S N M P Y A L L S S S V S F Y L P L L V M L 218
TTC GTC TAT GCT CGA GTG TTC GTT GCT AAG CGC CAA CGG CAT TTG CTG CGC GAA CTG GGC CGC TTC TCG CCC GAG GAG TCT CCG 1311
F V Y A R V F V A K R Q R H L L R E L G R F S P E S P 248
CCG TCT CCG TCG CGC TCT CCG TCC CCT CCG GAA CAC CGC GCG ACC TTA GGT CTC ATT ATG GGC ATC TTC TCT CTG TGC TGG CTG CCC TTC TTC CTG GCC 1401
P S P S R S P S P A T G G T P A A P D G V P P C G R R P A R 278
CTC CTG CCA CTC CGG GAA CAC CGC GCG CCT CCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG GCG 1491
L L P L R E H R A L R T L G L I M G I F S L C W L P F F L A 308
AAC GTG CTG CGC GCA CTC GCG GGG CCC TCT CTA GTT CCC AGC GGA GTT TTC ATC GGC CTG AAC TGG GGC TAT GCC AAC TCC GCC TTC 1581
N V L R A L A G P S L V P S G V F I A L N W L G Y A N S A F 338
AAC CCG GTC ATC TAC TGC CGC AGC CCG GAC TTT CGC GAC GCC TTC CGT CTT CTG TGT AGC TAC GGT GGC CGT GGA CCG GAG GAG CCA 1671
N P V I Y C R S P D F R D A F R R L L C S Y G G R G P E P 368
CGC GCA GTC ACC TTC CCA GCC AGC CCT GTT GAA GCC AGG CAG AGT CCA CCG CTC AAC AG, gtaggggacacagcgggggaccggaggtctctggtgggga 1771
R A V T F P A S P V E A R Q S P P L N R Donor 1 387

FIG. 2A



Applicant(s) Laurent EMORINE et al.
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HUMAN AND MOUSE BETA3-ADRENERGIC
RECEPTOR GENES"
5 of 7 sheets

AMINO-ACID SEQUENCE OF THE HUMAN B3-ADRENERGIC RECEPTOR GENE

10	20	30	40	50	60	70	80
MAPWPHENSS	LAPWPD LPTL	APNTANTSGL	PGVPWEAALA	GALLALAVLA	TVGGNLLVIV	AIAWTPRLQT	MTNVFVTS LA
90	100	110	120	130	140	150	160
AADLVMGLLV	VPPAATLALT	GHWPLGATGC	ELWTSVDVLC	VTASIELTCA	LAVDRYLAVT	NPLRYGALVT	KRCARTAVVL
170	180	190	200	210	220	230	240
VWVVSAAVSF	APIMSQWWRV	GADAEAQRCH	SNPRCCAFAS	NMPYVLLSSS	VSFYLPLLVM	LFVYARVFVV	ATRQLRLLRG
250	260	270	280	290	300	310	320
ELGRFPPEES	PPAPSRSLAP	APVGTCAPPE	GVPACGRRPA	RLLPLREHRA	LCTLGLIMGT	FTLCWLPFFL	ANVLRALGGP
330	340	350	360	370	380	390	400
SLVPGPAFLA	LNWLG YANSA	FNPLIYCRSP	DFRSAFRRL L	CRCGRRLPPE	PCAAARPALF	PSGVPAARSS	PAQPRLCQRL
DGASWGV S							

FIG. 3

AMINO-ACID SEQUENCE OF THE MOUSE B3-ADRENERGIC RECEPTOR GENE

10	20	30	40	50	60	70	80
MAPWPHRNGS	LALWSDAPTL	DPSAANTSGL	PGVPWAAALA	GALLALATVG	GNLLVIIAIA	RTPLRQTITN	VFVTS LAAAD
90	100	110	120	130	140	150	160
LVVGLLVMP P	GATLALTGHW	PLGETGCELW	TSVDVLCVTA	SIETLCALAV	DRYLAVTNPL	RYGTLVTKRR	ARAAVVLVWI
170	180	190	200	210	220	230	240
VSAAVSFAPI	MSQWWRVGAD	AEAQECHSNP	RCCSFASNMP	YALLSSSVSF	YLPLLVM LFV	YARVFVVAKR	QRHLLRREL G
250	260	270	280	290	300	310	320
RFSPEESP PS	PSRSPSPATG	GTPAAPDGVP	PCGRRPARLL	PLREHRALRT	LGLIMGIFSL	CWLPFFLANV	LRALAGPSLV
330	340	350	360	370	380	390	400
PSGVFIALNW	LG YANSAFNP	VIYCRSPDFR	DAFRRL LCSY	GGRGPPEEPA	VTFPAS PVEA	RQSPPLNRFD	GYEGARPFPT

FIG. 4



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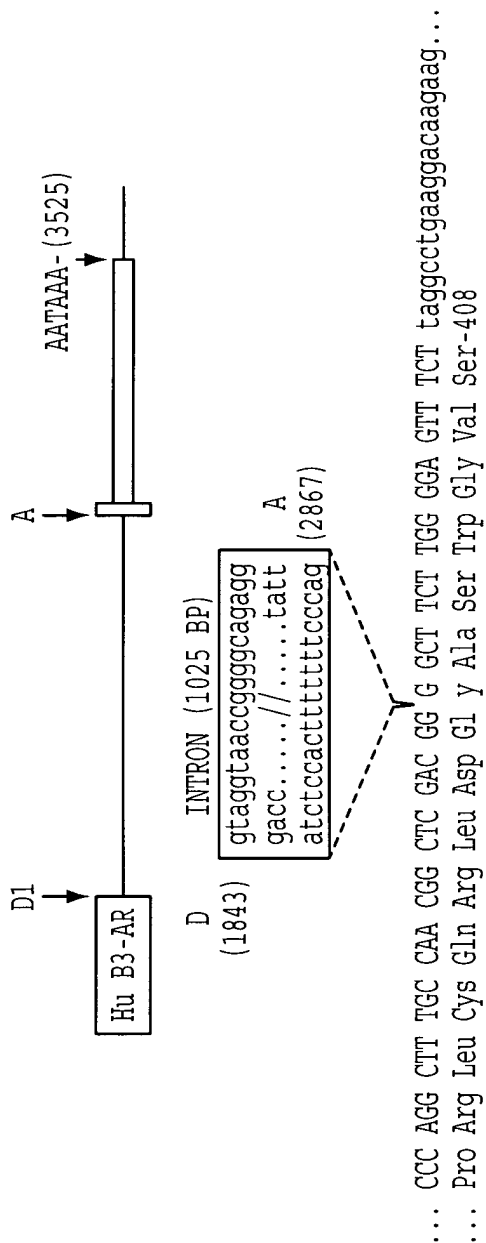


FIG. 5A

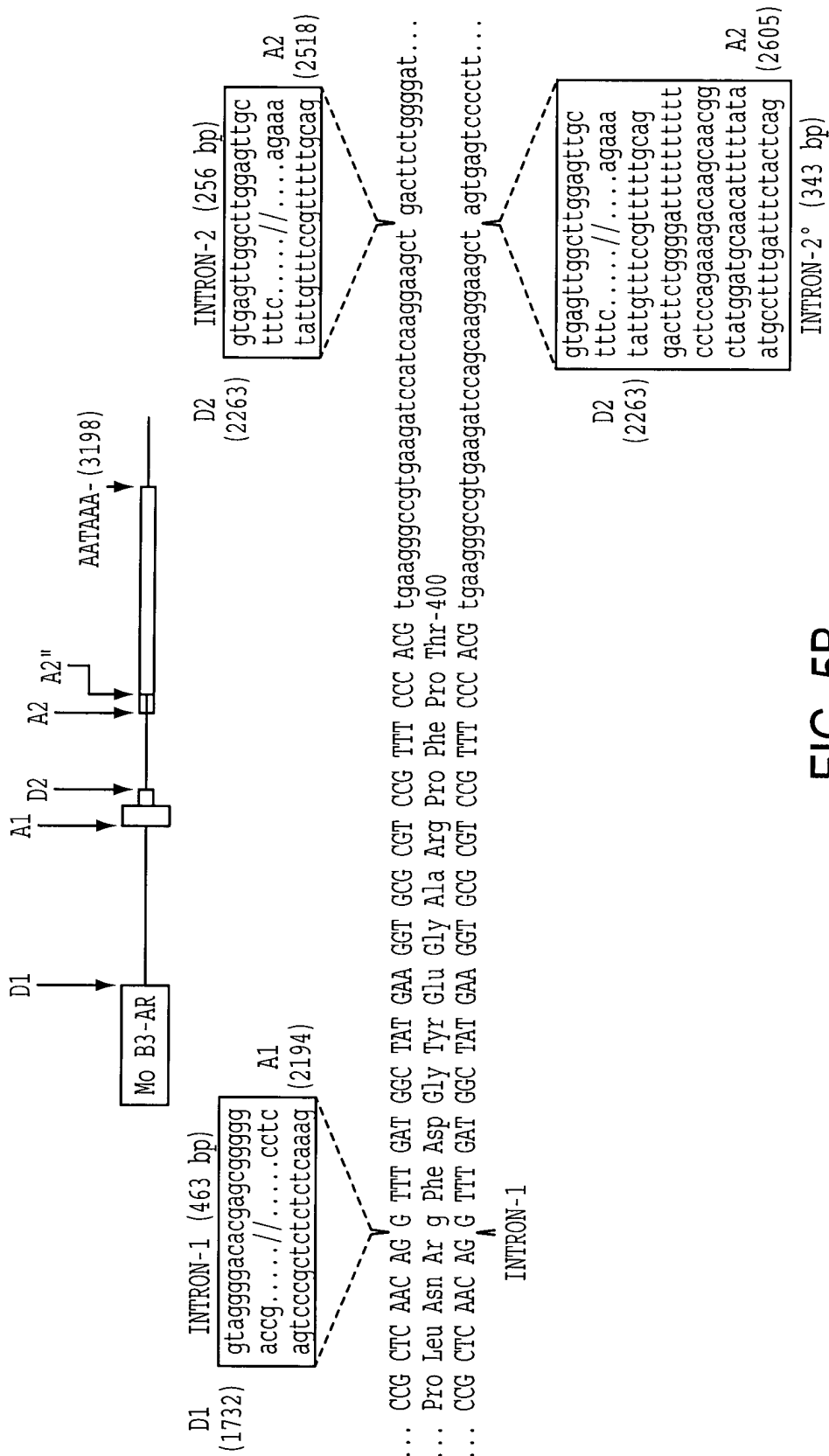


FIG. 5B